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#8

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/920,653

DATE: 11/06/2001

TIME: 11:59:53

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\11062001\I920653.raw

3 <110> APPLICANT: Japan as Represented by Director General of Okazaki National Research  
4 Institutes  
6 <120> TITLE OF INVENTION: Nav2 channel gene-deficient non-human animals  
8 <130> FILE REFERENCE: U2001P059  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/920,653  
C--> 11 <141> CURRENT FILING DATE: 2001-10-16  
13 <150> PRIOR APPLICATION NUMBER: JP 2000/237320  
14 <151> PRIOR FILING DATE: 2000-08-04  
16 <150> PRIOR APPLICATION NUMBER: JP 2000/241637  
17 <151> PRIOR FILING DATE: 2000-08-09  
19 <150> PRIOR APPLICATION NUMBER: JP 2001/222263  
20 <151> PRIOR FILING DATE: 2001-07-23  
22 <160> NUMBER OF SEQ ID NOS: 8  
24 <170> SOFTWARE: PatentIn Ver. 2.1  
26 <210> SEQ ID NO: 1  
27 <211> LENGTH: 446  
28 <212> TYPE: DNA  
29 <213> ORGANISM: Rattus norvegicus  
31 <400> SEQUENCE: 1  
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33 ataaaaaatc acattgctaa aaaatgcaac gaagagcatg aagaagaaga tttaaaacca 120  
34 agccgggata tagaagcagg caaaaaactt ccatttgctt atggaaccct tcctcaagga 180  
35 accgtgtcag agcccttgga agatgtggat ccatactact atgttaagag aaatactttc 240  
36 atggtcttaa acagaaacag agtcatcttc aggttcaatg cggtttccat cctctgcacg 300  
37 ttgtctcctt taagctctct cagaagagct gttatcaagg ttttggtgca ccccttttg 360  
38 cgctgtctga ttttaattag tgttctcacc gacagcatac ttatgtgcat gagtaacct 420  
39 ccggaatgga tattggcagt agagaa 446  
42 <210> SEQ ID NO: 2  
43 <211> LENGTH: 5482  
44 <212> TYPE: DNA  
45 <213> ORGANISM: Mus musculus  
47 <220> FEATURE:  
48 <221> NAME/KEY: CDS  
49 <222> LOCATION: (252)..(5297)  
51 <400> SEQUENCE: 2  
52 cagcgctcga ctagtacggg ggggggggag gggttggtct gtaggtggtc tctgggtctg 60  
54 tggagctagc ctggtggctg agtgttttagc tggagcagc agtggaccgc aaccacattg 120  
56 caacaacctc cgtagtagag atctgagaag acaagcccag gagagcaaag ggctctcgtg 180  
58 agccttgcat ctggggttct tgcctggagt ttatgtgaaga ctatgatttg acagcaacta 240  
60 taaaaccgaa a atg ttg act tcc cca gag ccg aag ggc ctt gtc cca ttt 290  
61 Met Leu Thr Ser Pro Glu Pro Lys Gly Leu Val Pro Phe  
62 1 5 10  
64 aca aca gag tca ctt gaa ctt ata gaa aat cac att gct aaa aaa tgc 338  
65 Thr Thr Glu Ser Leu Glu Ile Glu Asn His Ile Ala Lys Lys Cys  
66 15 20 25  
68 aat gaa gac ccc gaa gaa gaa gaa ggt tta aaa cca agt cgt aat cta 386  
69 Asn Glu Asp Pro Glu Glu Glu Glu Gly Leu Lys Pro Ser Arg Asn Leu

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70 30          35          40          45
72 gaa gct ggc aaa aga ctt cca att ccc tat gga acc ctc cct cga gga 434
73 Glu Ala Gly Lys Arg Leu Pro Ile Pro Tyr Gly Thr Leu Pro Arg Gly
74          50          55          60
76 acc gtg tca gag ccc ttg gaa gat gtg gat cca tac tac tat gtt aag 482
77 Thr Val Ser Glu Pro Leu Glu Asp Val Asp Pro Tyr Tyr Tyr Val Lys
78          65          70          75
80 aga aat act ttc atg gtc tta aac aga agc aga gtc atc ttc agg ttc 530
81 Arg Asn Thr Phe Met Val Leu Asn Arg Ser Arg Val Ile Phe Arg Phe
82          80          85          90
84 aat gcg gtt tcc atc ttc tgc aca ttg tct cct cta aac tcc ctc aga 578
85 Asn Ala Val Ser Ile Phe Cys Thr Leu Ser Pro Leu Asn Ser Leu Arg
86          95          100          105
88 aga gca gct atc aag gct ttg gtg cat ccc ctt ttt cgc ctg ctg att 626
89 Arg Ala Ala Ile Lys Ala Leu Val His Pro Leu Phe Arg Leu Leu Ile
90 110          115          120          125
92 tta atc agc gtt ctc act gac agc ata ctt atg tgc atg agt aat cta 674
93 Leu Ile Ser Val Leu Thr Asp Ser Ile Leu Met Cys Met Ser Asn Leu
94          130          135          140
96 cca gaa tgg ata ttg gca ata gag aat act ttg ctt ggg att tac gca 722
97 Pro Glu Trp Ile Leu Ala Ile Glu Asn Thr Leu Leu Gly Ile Tyr Ala
98          145          150          155
100 ttt gaa ata ctt gta aaa gtc att gca aga ggt atc tgg gca ggt tca 770
101 Phe Glu Ile Leu Val Lys Val Ile Ala Arg Gly Ile Trp Ala Gly Ser
102          160          165          170
104 ttt tcc ttc ctt ggg gat ctt tgg aac tgg ctt gat ttc agt gta act 818
105 Phe Ser Phe Leu Gly Asp Leu Trp Asn Trp Leu Asp Phe Ser Val Thr
106          175          180          185
108 ttg ttc gag cta atc aca agg ttt tca cct cta agc tcc ttt tta atg 866
109 Leu Phe Glu Leu Ile Thr Arg Phe Ser Pro Leu Ser Ser Phe Leu Met
110 190          195          200          205
112 ctt aaa act atc aga act ttc cga att ttg aag att atc cct ttg aac 914
113 Leu Lys Thr Ile Arg Thr Phe Arg Ile Leu Lys Ile Ile Pro Leu Asn
114          210          215          220
116 cac ggc ctg cag tct att gtg atg aca ctg gcc cag tgt ttg aag aaa 962
117 His Gly Leu Gln Ser Ile Val Met Thr Leu Ala Gln Cys Leu Lys Lys
118          225          230          235
120 cta ttt ggt gcc att gcc cta gct ctg ttt ttt ctg gct gtg ttt tca 1010
121 Leu Phe Gly Ala Ile Ala Leu Ala Leu Phe Phe Leu Ala Val Phe Ser
122          240          245          250
124 cta ctt gga atg ggc ctc ttc atg ggc aac ctg aag cac aaa tgt ctg 1058
125 Leu Leu Gly Met Gly Leu Phe Met Gly Asn Leu Lys His Lys Cys Leu
126          255          260          265
128 cgg tgg cca gaa gaa aat gaa aat gaa acg ctg cac aac aga act gga 1106
129 Arg Trp Pro Glu Glu Asn Glu Asn Glu Thr Leu His Asn Arg Thr Gly
130 270          275          280          285
132 agc ctt aac tat agt cca gaa aga ata aac ttc tac tac atg gaa gga 1154
133 Ser Leu Asn Tyr Ser Pro Glu Arg Ile Asn Phe Tyr Tyr Met Glu Gly
134          290          295          300

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136	gcg	aaa	tat	gct	ctc	ctt	tgc	ggc	aac	agg	aca	gat	gct	ggc	cag	tgt	1202
137	Ala	Lys	Tyr	Ala	Leu	Leu	Cys	Gly	Asn	Arg	Thr	Asp	Ala	Gly	Gln	Cys	
138				305				310						315			
140	ccg	gaa	ggt	tat	gtg	tgt	gta	aaa	gaa	ggc	aca	aat	cct	gac	aat	ggc	1250
141	Pro	Glu	Gly	Tyr	Val	Cys	Val	Lys	Glu	Gly	Thr	Asn	Pro	Asp	Asn	Gly	
142				320				325						330			
144	ttc	aca	agt	ttt	gac	aac	ttt	ggc	tgg	tcc	ctt	ctt	gct	atg	ttt	cga	1298
145	Phe	Thr	Ser	Phe	Asp	Asn	Phe	Gly	Trp	Ser	Leu	Leu	Ala	Met	Phe	Arg	
146				335				340						345			
148	ttg	atg	aca	cag	gat	tac	cct	gaa	tta	ctt	tat	cac	cag	atc	ctt	tat	1346
149	Leu	Met	Thr	Gln	Asp	Tyr	Pro	Glu	Leu	Leu	Tyr	His	Gln	Ile	Leu	Tyr	
150	350					355					360					365	
152	gct	tca	gga	aag	gtc	tac	atg	ata	ttt	ttt	ggt	atg	atc	agt	ttc	tgg	1394
153	Ala	Ser	Gly	Lys	Val	Tyr	Met	Ile	Phe	Phe	Val	Met	Ile	Ser	Phe	Trp	
154				370					375						380		
156	ttt	gcc	ttc	tat	ttg	aca	agt	ttg	ttc	ttg	ggc	ata	ctc	act	atg	acc	1442
157	Phe	Ala	Phe	Tyr	Leu	Thr	Ser	Leu	Phe	Leu	Gly	Ile	Leu	Thr	Met	Thr	
158				385					390						395		
160	tat	gaa	aag	gaa	aag	cag	aga	gcc	tgt	gag	gaa	tct	gga	ggc	ctt	gat	1490
161	Tyr	Glu	Lys	Glu	Lys	Gln	Arg	Ala	Cys	Glu	Glu	Ser	Gly	Gly	Leu	Asp	
162				400				405						410			
164	ccc	aaa	tgt	caa	cag	aca	gtg	aaa	gaa	ctc	gac	gaa	gaa	aat	gac	gca	1538
165	Pro	Lys	Cys	Gln	Gln	Thr	Val	Lys	Glu	Leu	Asp	Glu	Glu	Asn	Asp	Ala	
166				415				420						425			
168	gct	gag	atg	gaa	act	aca	caa	ata	gaa	atg	aag	aaa	aga	tcc	cca	act	1586
169	Ala	Glu	Met	Glu	Thr	Thr	Gln	Ile	Glu	Met	Lys	Lys	Arg	Ser	Pro	Thr	
170	430					435					440					445	
172	tct	ata	aac	acc	aca	ctg	gat	ata	ctg	gaa	gac	act	acc	ctc	gga	cac	1634
173	Ser	Ile	Asn	Thr	Thr	Leu	Asp	Ile	Leu	Glu	Asp	Thr	Thr	Leu	Gly	His	
174				450					455						460		
176	aga	gaa	gaa	cca	gaa	aca	tcc	agg	aag	aaa	tgc	cca	ata	tgt	tgg	cat	1682
177	Arg	Glu	Glu	Pro	Glu	Thr	Ser	Arg	Lys	Lys	Cys	Pro	Ile	Cys	Trp	His	
178				465					470						475		
180	aag	ttt	att	aaa	acc	tgc	ttc	atc	tgg	aaa	tgc	tct	ccc	tgt	tgg	gta	1730
181	Lys	Phe	Ile	Lys	Thr	Cys	Phe	Ile	Trp	Lys	Cys	Ser	Pro	Cys	Trp	Val	
182				480					485						490		
184	aaa	ctg	aac	gag	ttt	gct	gat	aga	ggt	ata	aca	cac	cca	ttg	gct	gat	1778
185	Lys	Leu	Asn	Glu	Phe	Ala	Asp	Arg	Val	Ile	Thr	His	Pro	Leu	Ala	Asp	
186				495				500						505			
188	ctt	ttt	ctt	gtc	atc	tgc	atc	ggt	tta	aac	ata	tgc	ttc	ctc	gcc	cta	1826
189	Leu	Phe	Leu	Val	Ile	Cys	Ile	Val	Leu	Asn	Ile	Cys	Phe	Leu	Ala	Leu	
190	510					515					520					525	
192	gaa	cat	ttt	cca	atg	agc	gag	gag	ctc	agg	tct	ctc	ctt	cac	gtt	gga	1874
193	Glu	His	Phe	Pro	Met	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Leu	His	Val	Gly	
194				530						535					540		
196	aat	ttg	ggt	ttt	att	gga	att	tac	aca	ata	gaa	ctg	att	ttg	aag	ata	1922
197	Asn	Leu	Val	Phe	Ile	Gly	Ile	Tyr	Thr	Ile	Glu	Leu	Ile	Leu	Lys	Ile	
198				545						550					555		
200	atc	gct	atg	cat	cca	tat	ggg	tat	ttt	caa	ata	agc	tgg	aat	att	ttt	1970

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201	Ile	Ala	Met	His	Pro	Tyr	Gly	Tyr	Phe	Gln	Ile	Ser	Trp	Asn	Ile	Phe	
202			560					565					570				
204	gac	agt	ata	ctt	gtg	ggt	ttg	gag	tta	aca	gaa	att	tta	cta	gca	gat	2018
205	Asp	Ser	Ile	Leu	Val	Val	Leu	Glu	Leu	Thr	Glu	Ile	Leu	Leu	Ala	Asp	
206		575					580					585					
208	ggt	gaa	gga	cta	gct	ggt	tta	ata	aca	gtc	cca	ttg	ata	ttt	ata	aaa	2066
209	Val	Glu	Gly	Leu	Ala	Val	Leu	Ile	Thr	Val	Pro	Leu	Ile	Phe	Ile	Lys	
210	590						595				600					605	
212	ctg	ggg	aag	tac	gga	cca	cca	ttt	aag	agt	ttg	atg	cgc	atc	ctt	ggt	2114
213	Leu	Gly	Lys	Tyr	Gly	Pro	Pro	Phe	Lys	Ser	Leu	Met	Arg	Ile	Leu	Gly	
214					610					615					620		
216	agc	tca	ttg	atg	gcc	ctg	aaa	gat	ttg	gtc	ctg	ttg	ctc	tgc	ata	ttc	2162
217	Ser	Ser	Leu	Met	Ala	Leu	Lys	Asp	Leu	Val	Leu	Leu	Leu	Cys	Ile	Phe	
218					625					630				635			
220	ggt	tac	ttc	tct	gct	gtg	ttc	ggc	atg	aag	ctg	ttt	ggt	cga	agt	tac	2210
221	Val	Tyr	Phe	Ser	Ala	Val	Phe	Gly	Met	Lys	Leu	Phe	Gly	Arg	Ser	Tyr	
222			640					645					650				
224	aag	gat	tgt	gtc	tgc	cac	ata	aag	gaa	gac	tgc	caa	ccc	caa	cgc	tgg	2258
225	Lys	Asp	Cys	Val	Cys	His	Ile	Lys	Glu	Asp	Cys	Gln	Pro	Gln	Arg	Trp	
226		655					660					665					
228	cac	atg	agt	gac	ttc	ctt	cat	gcc	tac	atg	acc	gtg	ttc	cga	atc	ctc	2306
229	His	Met	Ser	Asp	Phe	Leu	His	Ala	Tyr	Met	Thr	Val	Phe	Arg	Ile	Leu	
230	670					675					680					685	
232	tgt	gga	gag	tgg	ata	gag	aca	tta	tgg	gag	tgt	atg	gag	ggt	gca	ggc	2354
233	Cys	Gly	Glu	Trp	Ile	Glu	Thr	Leu	Trp	Glu	Cys	Met	Glu	Val	Ala	Gly	
234					690					695					700		
236	cag	gcc	tgg	tgt	att	cct	ttt	tac	atg	atg	gtc	att	tta	att	gga	aac	2402
237	Gln	Ala	Trp	Cys	Ile	Pro	Phe	Tyr	Met	Met	Val	Ile	Leu	Ile	Gly	Asn	
238					705					710					715		
240	tta	ttg	ata	ctt	tac	ctc	ttt	gtg	aca	ttg	gtg	agc	tct	ttc	agt	tac	2450
241	Leu	Leu	Ile	Leu	Tyr	Leu	Phe	Val	Thr	Leu	Val	Ser	Ser	Phe	Ser	Tyr	
242			720					725					730				
244	tat	gat	gct	aca	tcg	gaa	gtg	aac	aaa	gaa	gcc	aaa	aac	ctt	cag	ctt	2498
245	Tyr	Asp	Ala	Thr	Ser	Glu	Val	Asn	Lys	Glu	Ala	Lys	Asn	Leu	Gln	Leu	
246		735					740					745					
248	gcc	atg	gca	agg	ata	aag	tcg	gga	ata	aac	tcc	atg	ctt	ctt	aaa	tta	2546
249	Ala	Met	Ala	Arg	Ile	Lys	Ser	Gly	Ile	Asn	Ser	Met	Leu	Leu	Lys	Leu	
250	750					755					760					765	
252	atg	tgc	aca	gaa	aga	agt	ggt	cct	aca	gaa	gca	aca	gac	caa	ata	tgt	2594
253	Met	Cys	Thr	Glu	Arg	Ser	Val	Pro	Thr	Glu	Ala	Thr	Asp	Gln	Ile	Cys	
254					770					775					780		
256	gat	cca	agt	ggt	aaa	gag	aat	att	tct	ggc	cat	act	ctt	tct	gaa	ctg	2642
257	Asp	Pro	Ser	Val	Lys	Glu	Asn	Ile	Ser	Gly	His	Thr	Leu	Ser	Glu	Leu	
258					785					790					795		
260	agc	aac	acc	caa	act	ttc	ctc	aga	tat	aag	gac	cag	agc	agc	agc	act	2690
261	Ser	Asn	Thr	Gln	Thr	Phe	Leu	Arg	Tyr	Lys	Asp	Gln	Ser	Ser	Ser	Thr	
262			800					805					810				
264	gag	aaa	act	cca	gtg	act	gaa	tct	gag	agt	caa	tct	ctg	att	gct	agt	2738
265	Glu	Lys	Thr	Pro	Val	Thr	Glu	Ser	Glu	Ser	Gln	Ser	Leu	Ile	Ala	Ser	

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268	ccc agt gcc tct gaa act gtg ccg att gct tca gga gaa tct gat ata	2786		
269	Pro Ser Ala Ser Glu Thr Val Pro Ile Ala Ser Gly Glu Ser Asp Ile			
270	830 835 840 845			
272	gaa aat ctg gat aac aag gag act cgg agc aag tct ggg aat gga ggc	2834		
273	Glu Asn Leu Asp Asn Lys Glu Thr Arg Ser Lys Ser Gly Asn Gly Gly			
274	850 855 860			
276	agt aaa gag aaa atg aag cag tct agc tca tct gag tgc agc aca gtt	2882		
277	Ser Lys Glu Lys Met Lys Gln Ser Ser Ser Ser Glu Cys Ser Thr Val			
278	865 870 875			
280	gat atc gct att tct gaa gaa gaa gaa atg gtc tat gaa cat gaa aag	2930		
281	Asp Ile Ala Ile Ser Glu Glu Glu Glu Met Val Tyr Glu His Glu Lys			
282	880 885 890			
284	tca aag ctt cat aaa aat ggt tat gaa cgc aaa tct tca act ggt caa	2978		
285	Ser Lys Leu His Lys Asn Gly Tyr Glu Arg Lys Ser Ser Thr Gly Gln			
286	895 900 905			
288	atc agt aga gaa tct agg aat gga aag att tgg aaa aac atc agg aaa	3026		
289	Ile Ser Arg Glu Ser Arg Asn Gly Lys Ile Trp Lys Asn Ile Arg Lys			
290	910 915 920 925			
292	act tgc tgc aag ata gta gag aac agc tgg ttt gag tgt ttc att ggc	3074		
293	Thr Cys Cys Lys Ile Val Glu Asn Ser Trp Phe Glu Cys Phe Ile Gly			
294	930 935 940			
296	ctg gtc act ctg ctc tgc aca ggc act ctg gct ctt gaa gac ata tat	3122		
297	Leu Val Thr Leu Leu Cys Thr Gly Thr Leu Ala Leu Glu Asp Ile Tyr			
298	945 950 955			
300	att gat cag aga aaa acc act aaa atc tta ctg gaa tat gcg gac atg	3170		
301	Ile Asp Gln Arg Lys Thr Thr Lys Ile Leu Leu Glu Tyr Ala Asp Met			
302	960 965 970			
304	ata ttt gca tac atc ttc att ctg gag atg ctt ctc aag tgg gtg gct	3218		
305	Ile Phe Ala Tyr Ile Phe Ile Leu Glu Met Leu Leu Lys Trp Val Ala			
306	975 980 985			
308	tat ggc ttt aaa gcc ttt ttc tcc aac aac tgg tac aaa ctg gac ttt	3266		
309	Tyr Gly Phe Lys Ala Phe Phe Ser Asn Asn Trp Tyr Lys Leu Asp Phe			
310	990 995 1000 1005			
312	atg gtt gtt atc gtg ttt tgt ctt agc tta ata ggc aaa act cga gaa	3314		
313	Met Val Val Ile Val Phe Cys Leu Ser Leu Ile Gly Lys Thr Arg Glu			
314	1010 1015 1020			
316	gat ctg aac cct ctg aca tca ata aag ttc ctt cga gca cta aga gtt	3362		
317	Asp Leu Asn Pro Leu Thr Ser Ile Lys Phe Leu Arg Ala Leu Arg Val			
318	1025 1030 1035			
320	ctg tgc cag ttt gaa aga atg aag gtg gtc ctg aga gct ttg ata aaa	3410		
321	Leu Ser Gln Phe Glu Arg Met Lys Val Val Leu Arg Ala Leu Ile Lys			
322	1040 1045 1050			
324	aca acc tta ccc act gtg agc gtg ttt cta gtc tgc cta atg atc tgg	3458		
325	Thr Thr Leu Pro Thr Val Ser Val Phe Leu Val Cys Leu Met Ile Trp			
326	1055 1060 1065			
328	ctg ctt ttc agt gtt att gga gtg cag tta ttt gct ggc aag ttc tat	3506		
329	Leu Leu Phe Ser Val Ile Gly Val Gln Leu Phe Ala Gly Lys Phe Tyr			
330	1070 1075 1080 1085			

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date